

**Amendments to the Claims**

Please cancel Claims 6, 7, 11-14, 21, 22 and 25-36. Please amend Claims 1, 3, 4, 15, 18, 19 and 37-40. The Claim Listing below will replace all prior versions of the claims in the application:

**Claim Listing**

1. (Currently amended) A method of classifying a lymphoma sample according to predicted treatment outcome comprising the steps of:
  - a) — isolating a gene expression product from two or more informative genes from one or more cells in said sample; and
  - b) — determining a gene expression profile of gene expression products from two or more of the informative genes, wherein the gene expression products are isolated from one or more cells in the sample, wherein the gene expression profile is correlated with a treatment outcome, thereby classifying the sample with respect to treatment outcome.
2. (Original) A method according to Claim 1, wherein the lymphoma sample is a diffuse large cell lymphoma sample.
3. (Currently amended) A method according to Claim 1, wherein the gene expression products are product is mRNA.
4. (Currently amended) A method according to Claim 3, wherein the gene expression profile is determined using hybridization probes specific to the two or more of the informative genes.
5. (Original) A method according to Claim 3, wherein the gene expression profile is determined using oligonucleotide microarrays.

6. and 7. (Canceled)

8. (Original) A method according to Claim 1, wherein the predicted treatment outcome is survival after treatment.

9. through 14. (Canceled)

9 15. (Currently amended) A method of classifying a sample according to lymphoma type comprising the steps of:

- a) — isolating a gene expression product from at least one informative gene from one or more cells in said sample; and
- b) — determining a gene expression profile of gene expression products from two or more of the informative genes, wherein the gene expression product is isolated from one or more cells in the sample,

wherein the gene expression profile is correlated with a lymphoma type, thereby classifying the sample with respect to lymphoma type.

10 16. (Original) A method according to Claim 15, <sup>9</sup> wherein the lymphoma type is diffuse large cell lymphoma.

11 17. (Original) A method according to Claim 15, <sup>9</sup> wherein the lymphoma type is follicular lymphoma.

12 18. (Currently amended) A method according to Claim 15, <sup>9</sup> wherein the gene expression products are product is mRNA.

13 19. (Currently amended) A method according to Claim 18, <sup>9</sup> wherein the gene expression profile is determined using hybridization probes specific to the two or more of the informative genes.

*14*  
20. (Original) A method according to Claim 18, wherein the gene expression profile is determined using oligonucleotide microarrays.

21. through 36. (Canceled)

*15 37.* (Currently amended) The method of Claim 1, wherein the a gene expression products are product is isolated from at least five informative genes from one or more cells in said sample and wherein a gene expression profile of said at least five informative genes is determined.

*16 38.* (Currently amended) The method of Claim 1, wherein the a gene expression products are product is isolated from at least ten informative genes from one or more cells in said sample and wherein a gene expression profile of said at least ten informative genes is determined.

*17 39.* (Currently amended) The method of Claim 15, wherein the a gene expression products are product is isolated from at least five informative genes from one or more cells in said sample and wherein a gene expression profile of said at least five informative genes is determined.

*18 40.* (Currently amended) The method of Claim 18, wherein the a gene expression products are product is isolated from at least ten informative genes from one or more cells in said sample and wherein a gene expression profile of said at least ten informative genes is determined.